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<110> CHUGAI RESEARCH INSTITUTE FOR MOLECULAR MEDICINE, INC.

<120> TRANSPORTER GENES

<130> C2-906DP1PCT

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<150> JP 9-260972
JP 10-156660
<151> 1997-9-8
1998-5-20

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<212> PRT
<213> Homo sapiens

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Met Arg Asp Tyr Asp Glu Val Ile Ala
1 5

Phe Leu Gly Glu Trp Gly Pro Phe Gln Arg Leu Ile Phe Phe Leu Leu
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Ser Ala Ser Ile Ile Pro Asn Gly Phe Asn Gly Met Ser Val Val Phe
30 35 40

Leu Ala Gly Thr Pro Glu His Arg Cys Arg Val Pro Asp Ala Ala Asn
45 50 55

Leu Ser Ser Ala Trp Arg Asn Asn Ser Val Pro Leu Arg Leu Arg Asp
60 65 70

Gly Arg Glu Val Pro His Ser Cys Ser Arg Tyr Arg Leu Ala Thr Ile
75 80 85

Ala Asn Phe Ser Ala Leu Gly Leu Glu Pro Gly Arg Asp Val Asp Leu

90 95 100 105

Gly Gln Leu Glu Gln Glu Ser Cys Leu Asp Gly Trp Glu Phe Ser Gln
110 115 120

Asp Val Tyr Leu Ser Thr Val Val Thr Glu Trp Asn Leu Val Cys Glu
125 130 135

Asp Asn Trp Lys Val Pro Leu Thr Thr Ser Leu Phe Phe Val Gly Val
140 145 150

sub A1)

Leu Leu Gly Ser Phe Val Ser Gly Gln Leu Ser Asp Arg Phe Gly Arg
155 160 165

Lys Asn Val Leu Phe Ala Thr Met Ala Val Gln Thr Gly Phe Ser Phe
170 175 180 185

Leu Gln Ile Phe Ser Ile Ser Trp Glu Met Phe Thr Val Leu Phe Val
190 195 200

A

Ile Val Gly Met Gly Gln Ile Ser Asn Tyr Val Val Ala Phe Ile Leu
205 210 215

Gly Thr Glu Ile Leu Gly Lys Ser Val Arg Ile Ile Phe Ser Thr Leu
220 225 230

Gly Val Cys Thr Phe Phe Ala Val Gly Tyr Met Leu Leu Pro Leu Phe
235 240 245

Ala Tyr Phe Ile Arg Asp Trp Arg Met Leu Leu Leu Ala Leu Thr Val
250 255 260 265

Pro Gly Val Leu Cys Val Pro Leu Trp Trp Phe Ile Pro Glu Ser Pro
270 275 280

Arg Trp Leu Ile Ser Gln Arg Arg Phe Arg Glu Ala Glu Asp Ile Ile
285 290 295

Gln Lys Ala Ala Lys Met Asn Asn Thr Ala Val Pro Ala Val Ile Phe
300 305 310

Asp Ser Val Glu Glu Leu Asn Pro Leu Lys Gln Gln Lys Ala Phe Ile
315 320 325

Leu Asp Leu Phe Arg Thr Arg Asn Ile Ala Ile Met Thr Ile Met Ser
330 335 340 345

Leu Leu Leu Trp Met Leu Thr Ser Val Gly Tyr Phe Ala Leu Ser Leu
350 355 360

Asp Ala Pro Asn Leu His Gly Asp Ala Tyr Leu Asn Cys Phe Leu Ser
365 370 375

Sub A1 Ala Leu Ile Glu Ile Pro Ala Tyr Ile Thr Ala Trp Leu Leu Leu Arg
380 385 390

Thr Leu Pro Arg Arg Tyr Ile Ile Ala Ala Val Leu Phe Trp Gly Gly
395 400 405

Gly Val Leu Leu Phe Ile Gln Leu Val Pro Val Asp Tyr Tyr Phe Leu
410 415 420 425

Ser Ile Gly Leu Val Met Leu Gly Lys Phe Gly Ile Thr Ser Ala Phe
430 435 440

Ser Met Leu Tyr Val Phe Thr Ala Glu Leu Tyr Pro Thr Leu Val Arg
445 450 455

Asn Met Ala Val Gly Val Thr Ser Thr Ala Ser Arg Val Gly Ser Ile
460 465 470

Ile Ala Pro Tyr Phe Val Tyr Leu Gly Ala Tyr Asn Arg Met Leu Pro
475 480 485

Tyr Ile Val Met Gly Ser Leu Thr Val Leu Ile Gly Ile Phe Thr Leu
490 495 500 505

Phe Phe Pro Glu Ser Leu Gly Met Thr Leu Pro Glu Thr Leu Glu Gln
510 515 520

Met Gln Lys Val Lys Trp Phe Arg Ser Gly Lys Lys Thr Arg Asp Ser
525 530 535

Met Glu Thr Glu Glu Asn Pro Lys Val Leu Ile Thr Ala Phe
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caagtttcgg agcggcagtg ggaagc atg cgg gac tac gac gag gtg atc gcc 173
Met Arg Asp Tyr Asp Glu Val Ile Ala
1 5

ttc ctg ggc gag tgg ggg ccc ttc cag cgc ctc atc ttc ttc ctg ctc 221
Phe Leu Gly Glu Trp Gly Pro Phe Gln Arg Leu Ile Phe Phe Leu Leu
10 15 20 25

agc gcc agc atc atc ccc aat ggc ttc aat ggt atg tca gtc gtg ttc 269
Ser Ala Ser Ile Ile Pro Asn Gly Phe Asn Gly Met Ser Val Val Phe
30 35 40

ctg gcg ggg acc ccg gag cac cgc tgt cga gtg ccg gac gcc gcg aac 317
Leu Ala Gly Thr Pro Glu His Arg Cys Arg Val Pro Asp Ala Ala Asn
45 50 55

ctg agc agc gcc tgg cgc aac aac agt gtc ccg ctg cgg ctg cgg gac 365
Leu Ser Ser Ala Trp Arg Asn Asn Ser Val Pro Leu Arg Leu Arg Asp
60 65 70

ggc cgc gag gtg ccc cac agc tgc agc cgc tac cgg ctc gcc acc atc 413
Gly Arg Glu Val Pro His Ser Cys Ser Arg Tyr Arg Leu Ala Thr Ile
75 80 85

gcc aac ttc tcg gcg ctc ggg ctg gag ccg ggg cgc gac gtg gac ctg 461
Ala Asn Phe Ser Ala Leu Gly Leu Glu Pro Gly Arg Asp Val Asp Leu
90 95 100 105

ggg cag ctg gag cag gag agc tgc ctg gat ggc tgg gag ttc agc cag 509

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Gly Gln Leu Glu Gln Glu Ser Cys Leu Asp Gly Trp Glu Phe Ser Gln
                110                 115                 120

gac gtc tac ctg tcc acc gtc gtg acc gag tgg aat ctg gtg tgt gag      557
Asp Val Tyr Leu Ser Thr Val Val Thr Glu Trp Asn Leu Val Cys Glu
            125                 130                 135

gac aac tgg aag gtg ccc ctc acc acc tcc ctg ttc ttc gta ggc gtg      605
Asp Asn Trp Lys Val Pro Leu Thr Thr Ser Leu Phe Phe Val Gly Val
        140                 145                 150

ctc ctc ggc tcc ttc gtg tcc ggg cag ctg tca gac agg ttt ggc agg      653
Leu Leu Gly Ser Phe Val Ser Gly Gln Leu Ser Asp Arg Phe Gly Arg
    155                 160                 165

aag aac gtt ctc ttc gca acc atg gct gta cag act ggc ttc agc ttc      701
Lys Asn Val Leu Phe Ala Thr Met Ala Val Gln Thr Gly Phe Ser Phe
170                 175                 180                 185

ctg cag att ttc tcc atc agc tgg gag atg ttc act gtg tta ttt gtc      749
Leu Gln Ile Phe Ser Ile Ser Trp Glu Met Phe Thr Val Leu Phe Val
                190                 195                 200

atc gtg ggc atg ggc cag atc tcc aac tat gtg gta gcc ttc ata cta      797
Ile Val Gly Met Gly Gln Ile Ser Asn Tyr Val Val Ala Phe Ile Leu
            205                 210                 215

gga aca gaa att ctt ggc aag tca gtt cgt att ata ttc tct aca tta      845
Gly Thr Glu Ile Leu Gly Lys Ser Val Arg Ile Ile Phe Ser Thr Leu
        220                 225                 230

gga gtg tgc aca ttt ttt gca gtt ggc tat atg ctg ctg cca ctg ttt      893
Gly Val Cys Thr Phe Phe Ala Val Gly Tyr Met Leu Leu Pro Leu Phe
    235                 240                 245

gct tac ttc atc aga gac tgg cgg atg ctg ctg ctg gcg ctg acg gtg      941
Ala Tyr Phe Ile Arg Asp Trp Arg Met Leu Leu Leu Ala Leu Thr Val
250                 255                 260                 265

ccg gga gtg ctg tgt gtc ccg ctg tgg tgg ttc att cct gaa tct ccc      989
Pro Gly Val Leu Cys Val Pro Leu Trp Trp Phe Ile Pro Glu Ser Pro
                270                 275                 280
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cga tgg ctg ata tcc cag aga aga ttt aga gag gct gaa gat atc atc      1037
Arg Trp Leu Ile Ser Gln Arg Arg Phe Arg Glu Ala Glu Asp Ile Ile
            285                 290                 295

caa aaa gct gca aaa atg aac aac aca gct gta cca gca gtg ata ttt      1085
Gln Lys Ala Ala Lys Met Asn Asn Thr Ala Val Pro Ala Val Ile Phe
        300                 305                 310

gat tct gtg gag gag cta aat ccc ctg aag cag cag aaa gct ttc att      1133
Asp Ser Val Glu Glu Leu Asn Pro Leu Lys Gln Gln Lys Ala Phe Ile
    315                 320                 325

ctg gac ctg ttc agg act cgg aat att gcc ata atg acc att atg tct      1181
Leu Asp Leu Phe Arg Thr Arg Asn Ile Ala Ile Met Thr Ile Met Ser
330                 335                 340                 345

ttg ctg cta tgg atg ctg acc tca gtg ggt tac ttt gct ctg tct ctg      1229
Leu Leu Leu Trp Met Leu Thr Ser Val Gly Tyr Phe Ala Leu Ser Leu
                350                 355                 360

gat gct cct aat tta cat gga gat gcc tac ctg aac tgt ttc ctc tct      1277
Asp Ala Pro Asn Leu His Gly Asp Ala Tyr Leu Asn Cys Phe Leu Ser
            365                 370                 375

gcc ttg att gaa att cca gct tac att aca gcc tgg ctg cta ttg cga      1325
Ala Leu Ile Glu Ile Pro Ala Tyr Ile Thr Ala Trp Leu Leu Leu Arg
        380                 385                 390

acg ctg ccc agg cgt tat atc ata gct gca gta ctg ttc tgg gga gga      1373
Thr Leu Pro Arg Arg Tyr Ile Ile Ala Ala Val Leu Phe Trp Gly Gly
    395                 400                 405

ggt gtg ctt ctc ttc att caa ctg gta cct gtg gat tat tac ttc tta      1421
Gly Val Leu Leu Phe Ile Gln Leu Val Pro Val Asp Tyr Tyr Phe Leu
410                 415                 420                 425

tcc att ggt ctg gtc atg ctg gga aaa ttt ggg atc acc tct gct ttc      1469
Ser Ile Gly Leu Val Met Leu Gly Lys Phe Gly Ile Thr Ser Ala Phe
                430                 435                 440

tcc atg ctg tat gtc ttc act gct gag ctc tac cca acc ctg gtc agg      1517
Ser Met Leu Tyr Val Phe Thr Ala Glu Leu Tyr Pro Thr Leu Val Arg
            445                 450                 455
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SubA1

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aac atg gcg gtg ggg gtc aca tcc acg gcc tcc aga gtg ggc agc atc     1565
Asn Met Ala Val Gly Val Thr Ser Thr Ala Ser Arg Val Gly Ser Ile
        460                 465                 470

att gcc ccc tac ttt gtt tac ctc ggt gct tac aac aga atg ctg ccc     1613
Ile Ala Pro Tyr Phe Val Tyr Leu Gly Ala Tyr Asn Arg Met Leu Pro
    475                 480                 485

tac atc gtc atg ggt agt ctg act gtc ctg att gga atc ttc acc ctt     1661
Tyr Ile Val Met Gly Ser Leu Thr Val Leu Ile Gly Ile Phe Thr Leu
490                 495                 500                 505

ttt ttc cct gaa agt ttg gga atg act ctt cca gaa acc tta gag cag     1709
Phe Phe Pro Glu Ser Leu Gly Met Thr Leu Pro Glu Thr Leu Glu Gln
                510                 515                 520

atg cag aaa gtg aaa tgg ttc aga tct ggg aaa aaa aca aga gac tca     1757
Met Gln Lys Val Lys Trp Phe Arg Ser Gly Lys Lys Thr Arg Asp Ser
            525                 530                 535

atg gag aca gaa gaa aat ccc aag gtt cta ata act gca ttc             1799
Met Glu Thr Glu Glu Asn Pro Lys Val Leu Ile Thr Ala Phe
        540                 545                 550

tgaaaaaata tctaccccat ttggtgaagt gaaaaacaga aaaataagac cctgtggaga   1859

aattcgttgt tcccactgaa atggactgac tgtaacgatt gacaccaaaa tgaaccttgc   1919

tatcaagaaa tgctcgtcat acagtaaact ctggatgatt cttccagata atgtccttgc   1979

tttacaaacc aaccatttct agagagtctc cttactcatt aattcaatga aatggattgg   2039

taagatgtct tgaaaacatg ttagtcaagg actggtaaaa tacatataaa gattaacact   2099

catttccaat catacaaata ctatccaaat aaaaat                             2135
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<213> Homo sapiens

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Asn Gly Phe Thr Gly Leu Ser Ser Val Phe Leu Ile Ala Thr Pro Glu
35 40 45

His Arg Cys Arg Val Pro Asp Ala Ala Asn Leu Ser Ser Ala Trp Arg
50 55 60

Asn His Thr Val Pro Leu Arg Leu Arg Asp Gly Arg Glu Val Pro His
65 70 75

Ser Cys Arg Arg Tyr Arg Leu Ala Thr Ile Ala Asn Phe Ser Ala Leu
80 85 90 95

Gly Leu Glu Pro Gly Arg Asp Val Asp Leu Gly Gln Leu Glu Gln Glu
100 105 110

Ser Cys Leu Asp Gly Trp Glu Phe Ser Gln Asp Val Tyr Leu Ser Thr
115 120 125

Ile Val Thr Glu Trp Asn Leu Val Cys Glu Asp Asp Trp Lys Ala Pro
130 135 140

Leu Thr Ile Ser Leu Phe Phe Val Gly Val Leu Leu Gly Ser Phe Ile
145 150 155

Ser Gly Gln Leu Ser Asp Arg Phe Gly Arg Lys Asn Val Leu Phe Val
160 165 170 175

Thr Met Gly Met Gln Thr Gly Phe Ser Phe Leu Gln Ile Phe Ser Lys
180 185 190

Asn Phe Glu Met Phe Val Val Leu Phe Val Leu Val Gly Met Gly Gln
195 200 205

Ile Ser Asn Tyr Val Ala Ala Phe Val Leu Gly Thr Glu Ile Leu Gly
210 215 220

Lys Ser Val Arg Ile Ile Phe Ser Thr Leu Gly Val Cys Ile Phe Tyr

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    225                 230                 235

Ala Phe Gly Tyr Met Val Leu Pro Leu Phe Ala Tyr Phe Ile Arg Asp
240                 245                 250                 255

Trp Arg Met Leu Leu Val Ala Leu Thr Met Pro Gly Val Leu Cys Val
                260                 265                 270

Ala Leu Trp Trp Phe Ile Pro Glu Ser Pro Arg Trp Leu Ile Ser Gln
            275                 280                 285

Gly Arg Phe Glu Glu Ala Glu Val Ile Ile Arg Lys Ala Ala Lys Ala
        290                 295                 300

Asn Gly Ile Val Val Pro Ser Thr Ile Phe Asp Pro Ser Glu Leu Gln
    305                 310                 315

Asp Leu Ser Ser Lys Lys Gln Gln Ser His Asn Ile Leu Asp Leu Leu
320                 325                 330                 335

Arg Thr Trp Asn Ile Arg Met Val Thr Ile Met Ser Ile Met Leu Trp
                340                 345                 350

Met Thr Ile Ser Val Gly Tyr Phe Gly Leu Ser Leu Asp Thr Pro Asn
            355                 360                 365

Leu His Gly Asp Ile Phe Val Asn Cys Phe Leu Ser Ala Met Val Glu
        370                 375                 380

Val Pro Ala Tyr Val Leu Ala Trp Leu Leu Leu Gln Tyr Leu Pro Arg
    385                 390                 395

Arg Tyr Ser Met Ala Thr Ala Leu Phe Leu Gly Gly Ser Val Leu Leu
400                 405                 410                 415

Phe Met Gln Leu Val Pro Pro Asp Leu Tyr Tyr Leu Ala Thr Val Leu
                420                 425                 430

Val Met Val Gly Lys Phe Gly Val Thr Ala Ala Phe Ser Met Val Tyr
            435                 440                 445

Val Tyr Thr Ala Glu Leu Tyr Pro Thr Val Val Arg Asn Met Gly Val
        450                 455                 460
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Gly Val Ser Ser Thr Ala Ser Arg Leu Gly Ser Ile Leu Ser Pro Tyr
    465                 470                 475

Phe Val Tyr Leu Gly Ala Tyr Asp Arg Phe Leu Pro Tyr Ile Leu Met
480                 485                 490                 495

Gly Ser Leu Thr Ile Leu Thr Ala Ile Leu Thr Leu Phe Leu Pro Glu
                500                 505                 510

Ser Phe Gly Thr Pro Leu Pro Asp Thr Ile Asp Gln Met Leu Arg Val
            515                 520                 525

Lys Gly Met Lys His Arg Lys Thr Pro Ser His Thr Arg Met Leu Lys
        530                 535                 540

Asp Gly Gln Glu Arg Pro Thr Ile Leu Lys Ser Thr Ala Phe
    545                 550                 555
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SUBA17

A

<210> 4
<211> 1831
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (124)..(1794)

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cacgcgcaaa gcccgccgcg ttcccagacc ccaggccgcg ctctgtgggc ctctgagggc    120

ggc atg cgg gac tac gac gag gtg acc gcc ttc ctg ggc gag tgg ggg      168
    Met Arg Asp Tyr Asp Glu Val Thr Ala Phe Leu Gly Glu Trp Gly
      1               5                  10                  15

ccc ttc cag cgc ctc atc ttc ttc ctg ctc agc gcc agc atc atc ccc      216
Pro Phe Gln Arg Leu Ile Phe Phe Leu Leu Ser Ala Ser Ile Ile Pro
                20                  25                  30

aat ggc ttc acc ggc ctg tcc tcc gtg ttc ctg ata gcg acc ccg gag      264
Asn Gly Phe Thr Gly Leu Ser Ser Val Phe Leu Ile Ala Thr Pro Glu
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                35                  40                  45

cac cgc tgc cgg gtg ccg gac gcc gcg aac ctg agc agc gcc tgg cgc      312
His Arg Cys Arg Val Pro Asp Ala Ala Asn Leu Ser Ser Ala Trp Arg
        50                  55                  60

aac cac act gtc cca ctg cgg ctg cgg gac ggc cgc gag gtg ccc cac      360
Asn His Thr Val Pro Leu Arg Leu Arg Asp Gly Arg Glu Val Pro His
    65                  70                  75

agc tgc cgc cgc tac cgg ctc gcc acc atc gcc aac ttc tcg gcg ctc      408
Ser Cys Arg Arg Tyr Arg Leu Ala Thr Ile Ala Asn Phe Ser Ala Leu
 80                  85                  90                  95

ggg ctg gag ccg ggg cgc gac gtg gac ctg ggg cag ctg gag cag gag      456
Gly Leu Glu Pro Gly Arg Asp Val Asp Leu Gly Gln Leu Glu Gln Glu
                100                 105                 110

agc tgt ctg gat ggc tgg gag ttc agt cag gac gtc tac ctg tcc acc      504
Ser Cys Leu Asp Gly Trp Glu Phe Ser Gln Asp Val Tyr Leu Ser Thr
            115                 120                 125

att gtg acc gag tgg aac ctg gtg tgt gag gac gac tgg aag gcc cca      552
Ile Val Thr Glu Trp Asn Leu Val Cys Glu Asp Asp Trp Lys Ala Pro
        130                 135                 140

ctc aca atc tcc ttg ttc ttc gtg ggt gtg ctg ttg ggc tcc ttc att      600
Leu Thr Ile Ser Leu Phe Phe Val Gly Val Leu Leu Gly Ser Phe Ile
    145                 150                 155

tca ggg cag ctg tca gac agg ttt ggc cgg aag aat gtg ctg ttc gtg      648
Ser Gly Gln Leu Ser Asp Arg Phe Gly Arg Lys Asn Val Leu Phe Val
160                 165                 170                 175

acc atg ggc atg cag aca ggc ttc agc ttc ctg cag atc ttc tcg aag      696
Thr Met Gly Met Gln Thr Gly Phe Ser Phe Leu Gln Ile Phe Ser Lys
                180                 185                 190

aat ttt gag atg ttt gtc gtg ctg ttt gtc ctt gta ggc atg ggc cag      744
Asn Phe Glu Met Phe Val Val Leu Phe Val Leu Val Gly Met Gly Gln
            195                 200                 205

atc tcc aac tat gtg gca gca ttt gtc ctg ggg aca gaa att ctt ggc      792
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Ile Ser Asn Tyr Val Ala Ala Phe Val Leu Gly Thr Glu Ile Leu Gly
210 215 220

aag tca gtt cgt ata ata ttc tct acg tta gga gtg tgc ata ttt tat 840
Lys Ser Val Arg Ile Ile Phe Ser Thr Leu Gly Val Cys Ile Phe Tyr
225 230 235

gca ttt ggc tac atg gtg ctg cca ctg ttt gct tac ttc atc cga gac 888
Ala Phe Gly Tyr Met Val Leu Pro Leu Phe Ala Tyr Phe Ile Arg Asp
240 245 250 255

SubA17

tgg cgg atg ctg ctg gtg gcg ctg acg atg ccg ggg gtg ctg tgc gtg 936
Trp Arg Met Leu Leu Val Ala Leu Thr Met Pro Gly Val Leu Cys Val
260 265 270

gca ctc tgg tgg ttc atc cct gag tcc ccc cga tgg ctc atc tct cag 984
Ala Leu Trp Trp Phe Ile Pro Glu Ser Pro Arg Trp Leu Ile Ser Gln
275 280 285

gga cga ttt gaa gag gca gag gtg atc atc cgc aag gct gcc aaa gcc 1032
Gly Arg Phe Glu Glu Ala Glu Val Ile Ile Arg Lys Ala Ala Lys Ala
290 295 300

aat ggg att gtt gtg cct tcc act atc ttt gac ccg agt gag tta caa 1080
Asn Gly Ile Val Val Pro Ser Thr Ile Phe Asp Pro Ser Glu Leu Gln
305 310 315

gac cta agt tcc aag aag cag cag tcc cac aac att ctg gat ctg ctt 1128
Asp Leu Ser Ser Lys Lys Gln Gln Ser His Asn Ile Leu Asp Leu Leu
320 325 330 335

cga acc tgg aat atc cgg atg gtc acc atc atg tcc ata atg ctg tgg 1176
Arg Thr Trp Asn Ile Arg Met Val Thr Ile Met Ser Ile Met Leu Trp
340 345 350

atg acc ata tca gtg ggc tat ttt ggg ctt tcg ctt gat act cct aac 1224
Met Thr Ile Ser Val Gly Tyr Phe Gly Leu Ser Leu Asp Thr Pro Asn
355 360 365

ttg cat ggg gac atc ttt gtg aac tgc ttc ctt tca gcg atg gtt gaa 1272
Leu His Gly Asp Ile Phe Val Asn Cys Phe Leu Ser Ala Met Val Glu
370 375 380

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gtc cca gca tat gtg ttg gcc tgg ctg ctg ctg caa tat ttg ccc cgg      1320
Val Pro Ala Tyr Val Leu Ala Trp Leu Leu Leu Gln Tyr Leu Pro Arg
    385                 390                 395

cgc tat tcc atg gcc act gcc ctc ttc ctg ggt ggc agt gtc ctt ctc      1368
Arg Tyr Ser Met Ala Thr Ala Leu Phe Leu Gly Gly Ser Val Leu Leu
400                 405                 410                 415

ttc atg cag ctg gta ccc cca gac ttg tat tat ttg gct aca gtc ctg      1416
Phe Met Gln Leu Val Pro Pro Asp Leu Tyr Tyr Leu Ala Thr Val Leu
                420                 425                 430

gtg atg gtg ggc aag ttt gga gtc acg gct gcc ttt tcc atg gtc tac      1464
Val Met Val Gly Lys Phe Gly Val Thr Ala Ala Phe Ser Met Val Tyr
            435                 440                 445

gtg tac aca gcc gag ctg tat ccc aca gtg gtg aga aac atg ggt gtg      1512
Val Tyr Thr Ala Glu Leu Tyr Pro Thr Val Val Arg Asn Met Gly Val
        450                 455                 460

gga gtc agc tcc aca gca tcc cgc ctg ggc agc atc ctg tct ccc tac      1560
Gly Val Ser Ser Thr Ala Ser Arg Leu Gly Ser Ile Leu Ser Pro Tyr
    465                 470                 475

ttc gtt tac ctt ggt gcc tac gac cgc ttc ctg ccc tac att ctc atg      1608
Phe Val Tyr Leu Gly Ala Tyr Asp Arg Phe Leu Pro Tyr Ile Leu Met
480                 485                 490                 495

gga agt ctg acc atc ctg aca gcc atc ctc acc ttg ttt ctc cca gag      1656
Gly Ser Leu Thr Ile Leu Thr Ala Ile Leu Thr Leu Phe Leu Pro Glu
                500                 505                 510

agc ttc ggt acc cca ctc cca gac acc att gac cag atg cta aga gtc      1704
Ser Phe Gly Thr Pro Leu Pro Asp Thr Ile Asp Gln Met Leu Arg Val
            515                 520                 525

aaa gga atg aaa cac aga aaa act cca agt cac aca agg atg tta aaa      1752
Lys Gly Met Lys His Arg Lys Thr Pro Ser His Thr Arg Met Leu Lys
        530                 535                 540

gat ggt caa gaa agg ccc aca atc ctt aaa agc aca gcc ttc              1794
Asp Gly Gln Glu Arg Pro Thr Ile Leu Lys Ser Thr Ala Phe
    545                 550                 555
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taacatcgct tccagtaagg gagaaactga agaggaa 1831

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<223> Description of Artificial Sequence: Artificial Synthesized Primer Seq
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<210> 6
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<210> 7
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<210> 8
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SUBA17

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<400> 15
agcatcctgt ctccctactt cgtt 24

<210> 16
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Artificial Synthesized Primer Seq
uence

<400> 16
gatggatccc ggacggtctt gggtcgcctg ctg 33

<210> 17
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Artificial Synthesized Primer Seq
uence

<400> 17
gatggatcca aatgctgcca catagttgga gat 33

<210> 18
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Artificial Synthesized Primer Seq
uence

<400> 18
gatggatcca tgggcatgca gacaggcttc agc 33

<210> 19

<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Artificial Synthesized Primer Seq
uence

<400> 19
gatggatcct tcctcttcag tttctccctt act 33

<210> 20
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Artificial Synthesized Primer Seq
uence

<400> 20
cgcgccgaat cgctgaatcc tttc 24

<210> 21
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Artificial Synthesized Primer Seq
uence

<400> 21
aggcttttga tttgttctgt tgag 24

<210> 22
<211> 553
<212> PRT
<213> Mus musculus

<400> 22
Met Arg Asp Tyr Asp Glu Val Ile Ala Phe Leu Gly Glu Trp Gly Pro

```
1               5                   10                  15
Phe Gln Arg Leu Ile Phe Phe Leu Leu Ser Ala Ser Ile Ile Pro Asn
            20                  25                  30
Gly Phe Asn Gly Met Ser Val Val Phe Leu Ala Gly Thr Pro Glu His
        35                  40                  45
Arg Cys Leu Val Pro Asp Thr Val Asn Leu Ser Ser Ser Trp Arg Asn
    50                  55                  60
His Ser Ile Pro Leu Glu Thr Lys Asp Gly Arg Gln Val Pro Gln Ser
65                  70                  75                  80
Cys Arg Arg Tyr Arg Leu Ala Thr Ile Ala Asn Phe Ser Ala Met Gly
                85                  90                  95
Leu Glu Pro Gly Gln Asp Val Asp Leu Glu Gln Leu Glu Gln Glu Ser
            100                 105                 110
Cys Leu Asp Gly Trp Glu Tyr Asp Lys Asp Ile Phe Leu Ser Thr Ile
        115                 120                 125
Val Thr Glu Trp Asn Leu Val Cys Glu Asp Asp Trp Lys Thr Pro Leu
    130                 135                 140
Thr Thr Ser Leu Phe Phe Val Gly Val Leu Cys Gly Ser Phe Val Ser
145                 150                 155                 160
Gly Gln Leu Ser Asp Arg Phe Gly Arg Lys Lys Val Leu Phe Ala Thr
                165                 170                 175
Met Ala Val Gln Thr Gly Phe Ser Phe Val Gln Ile Phe Ser Thr Asn
            180                 185                 190
Trp Glu Met Phe Thr Val Leu Phe Ala Ile Val Gly Met Gly Gln Ile
        195                 200                 205
Ser Asn Tyr Val Val Ala Phe Ile Leu Gly Thr Glu Ile Leu Ser Lys
    210                 215                 220
Ser Val Arg Ile Ile Phe Ser Thr Leu Gly Val Cys Thr Phe Phe Ala
225                 230                 235                 240
```

Sub A17

```
Ile Gly Tyr Met Val Leu Pro Leu Phe Ala Tyr Phe Ile Arg Asp Trp
            245                 250                 255

Arg Met Leu Leu Leu Ala Leu Thr Leu Pro Gly Leu Phe Cys Val Pro
        260                 265                 270

Leu Trp Trp Phe Ile Pro Glu Ser Pro Arg Trp Leu Ile Ser Gln Arg
    275                 280                 285

Arg Phe Ala Glu Ala Glu Gln Ile Ile Gln Lys Ala Ala Lys Met Asn
290                 295                 300

Ser Ile Val Ala Pro Ala Gly Ile Phe Asp Pro Leu Glu Leu Gln Glu
305                 310                 315                 320

Leu Asn Ser Leu Lys Gln Gln Lys Val Ile Ile Leu Asp Leu Phe Arg
                325                 330                 335

Thr Arg Asn Ile Ala Thr Ile Thr Val Met Ala Val Met Leu Trp Met
        340                 345                 350

Leu Thr Ser Val Gly Tyr Phe Ala Leu Ser Leu Asn Val Pro Asn Leu
    355                 360                 365

His Gly Asp Val Tyr Leu Asn Cys Phe Leu Ser Gly Leu Ile Glu Val
370                 375                 380

Pro Ala Tyr Phe Thr Ala Trp Leu Leu Leu Arg Thr Leu Pro Arg Arg
385                 390                 395                 400

Tyr Ile Ile Ala Gly Val Leu Phe Trp Gly Gly Gly Val Leu Leu Leu
                405                 410                 415

Ile Gln Val Val Pro Glu Asp Tyr Asn Phe Val Ser Ile Gly Leu Val
        420                 425                 430

Met Leu Gly Lys Phe Gly Ile Thr Ser Ala Phe Ser Met Leu Tyr Val
    435                 440                 445

Phe Thr Ala Glu Leu Tyr Pro Thr Leu Val Arg Asn Met Ala Val Gly
450                 455                 460
```

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Ile Thr Ser Met Ala Ser Arg Val Gly Ser Ile Ile Ala Pro Tyr Phe
465                 470                 475                 480

Val Tyr Leu Gly Ala Tyr Asn Arg Leu Leu Pro Tyr Ile Leu Met Gly
                485                 490                 495

Ser Leu Thr Val Leu Ile Gly Ile Ile Thr Leu Phe Phe Pro Glu Ser
            500                 505                 510

Phe Gly Val Thr Leu Pro Glu Asn Leu Glu Gln Met Gln Lys Val Arg
        515                 520                 525

Gly Phe Arg Cys Gly Lys Lys Ser Thr Val Ser Val Asp Arg Glu Glu
    530                 535                 540

Ser Pro Lys Val Leu Ile Thr Ala Phe
545                 550

<210> 23
<211> 2083
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (122)..(1780)

<400> 23
attcggcaca ggacggcgtg tttgacgagc cacctaggaa gatcccctca gcgcgccgaa    60

tcgctgaatc ctttctctcc acccacctcc ctcacgcaag ctgaggagga gaggtggaaa   120

c atg cgg gac tac gac gag gtg atc gcc ttc ctg ggc gag tgg ggg ccc   169
  Met Arg Asp Tyr Asp Glu Val Ile Ala Phe Leu Gly Glu Trp Gly Pro
    1               5                  10                  15
ttc cag cgc ctc atc ttc ttt ctg ctc agc gcc agc atc atc ccc aat    217
Phe Gln Arg Leu Ile Phe Phe Leu Leu Ser Ala Ser Ile Ile Pro Asn
            20                  25                  30

ggc ttc aat ggt atg tca gtc gtg ttc ctg gcg ggg acc ccc gag cac    265
Gly Phe Asn Gly Met Ser Val Val Phe Leu Ala Gly Thr Pro Glu His
        35                  40                  45
```

SUBA17

```
cgt tgc ctg gtt cct gac act gtg aac ctg agc agc tcc tgg cgc aac      313
Arg Cys Leu Val Pro Asp Thr Val Asn Leu Ser Ser Ser Trp Arg Asn
    50                  55                  60

cac agc atc ccc ttg gag acg aag gac gga cga cag gtg cct cag agc      361
His Ser Ile Pro Leu Glu Thr Lys Asp Gly Arg Gln Val Pro Gln Ser
65                  70                  75                  80

tgc cgc cgc tac cga ctg gcc acc atc gcc aac ttc tct gcg atg ggg      409
Cys Arg Arg Tyr Arg Leu Ala Thr Ile Ala Asn Phe Ser Ala Met Gly
                85                  90                  95

ctg gag cca gga cag gac gtg gat ctg gag cag ctg gag cag gag agc      457
Leu Glu Pro Gly Gln Asp Val Asp Leu Glu Gln Leu Glu Gln Glu Ser
            100                 105                 110

tgc ctg gat ggc tgg gag tac gac aag gac atc ttc ctg tcc acc atc      505
Cys Leu Asp Gly Trp Glu Tyr Asp Lys Asp Ile Phe Leu Ser Thr Ile
        115                 120                 125

gtg aca gag tgg aat ctg gtg tgt gag gat gac tgg aag aca ccc ctc      553
Val Thr Glu Trp Asn Leu Val Cys Glu Asp Asp Trp Lys Thr Pro Leu
    130                 135                 140

acc acc tcc ctg ttc ttc gta ggc gtt ctc tgc ggc tcc ttc gtg tct      601
Thr Thr Ser Leu Phe Phe Val Gly Val Leu Cys Gly Ser Phe Val Ser
145                 150                 155                 160

ggg cag ctg tca gac agg ttt ggc agg aag aaa gtc ctc ttt gca acc      649
Gly Gln Leu Ser Asp Arg Phe Gly Arg Lys Lys Val Leu Phe Ala Thr
                165                 170                 175

atg gct gtg cag act gga ttc agc ttc gtg cag att ttc tca acc aac      697
Met Ala Val Gln Thr Gly Phe Ser Phe Val Gln Ile Phe Ser Thr Asn
            180                 185                 190

tgg gag atg ttc act gtg ttg ttt gcc att gtg ggc atg ggc cag atc      745
Trp Glu Met Phe Thr Val Leu Phe Ala Ile Val Gly Met Gly Gln Ile
        195                 200                 205

tcc aac tac gtg gtg gcc ttc ata cta gga act gaa atc ctg agc aag      793
Ser Asn Tyr Val Val Ala Phe Ile Leu Gly Thr Glu Ile Leu Ser Lys
    210                 215                 220
```

```
tcg gtt cgc atc atc ttc tcc aca tta gga gtc tgt aca ttt ttt gca     841
Ser Val Arg Ile Ile Phe Ser Thr Leu Gly Val Cys Thr Phe Phe Ala
225                 230                 235                 240

atc ggc tac atg gtc ctg ccg ctg ttt gca tac ttc atc aga gac tgg     889
Ile Gly Tyr Met Val Leu Pro Leu Phe Ala Tyr Phe Ile Arg Asp Trp
                245                 250                 255

agg atg ctg ctg ctg gcc ctg aca ctg cct ggc ctg ttc tgt gtt ccc     937
Arg Met Leu Leu Leu Ala Leu Thr Leu Pro Gly Leu Phe Cys Val Pro
            260                 265                 270

ctg tgg tgg ttt att cca gaa tct ccc cgg tgg ctg ata tcc cag agg     985
Leu Trp Trp Phe Ile Pro Glu Ser Pro Arg Trp Leu Ile Ser Gln Arg
        275                 280                 285

aga ttt gca gag gcc gaa cag atc atc cag aaa gcc gca aag atg aac    1033
Arg Phe Ala Glu Ala Glu Gln Ile Ile Gln Lys Ala Ala Lys Met Asn
    290                 295                 300

agc atc gtg gcg cca gca ggg ata ttc gat cct cta gag cta cag gag    1081
Ser Ile Val Ala Pro Ala Gly Ile Phe Asp Pro Leu Glu Leu Gln Glu
305                 310                 315                 320

cta aac tcc ttg aag cag cag aaa gtc ata atc ctg gac ctg ttc agg    1129
Leu Asn Ser Leu Lys Gln Gln Lys Val Ile Ile Leu Asp Leu Phe Arg
                325                 330                 335

act cgg aac att gcc acc ata acc gtg atg gct gtg atg ctg tgg atg    1177
Thr Arg Asn Ile Ala Thr Ile Thr Val Met Ala Val Met Leu Trp Met
            340                 345                 350

cta acc tca gtg ggt tac ttt gct ctg tct ctc aat gtt cct aat tta    1225
Leu Thr Ser Val Gly Tyr Phe Ala Leu Ser Leu Asn Val Pro Asn Leu
        355                 360                 365

cat gga gat gtc tac ctg aac tgc ttc ctc tct ggc ctg att gaa gtt    1273
His Gly Asp Val Tyr Leu Asn Cys Phe Leu Ser Gly Leu Ile Glu Val
    370                 375                 380

cca gct tac ttc aca gcc tgg ctg cta ctg cga acc ctg cca cgg aga    1321
Pro Ala Tyr Phe Thr Ala Trp Leu Leu Leu Arg Thr Leu Pro Arg Arg
```

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385                 390                 395                 400

tat att ata gct ggg gtg cta ttc tgg gga gga ggt gtg ctt ctc ttg    1369
Tyr Ile Ile Ala Gly Val Leu Phe Trp Gly Gly Gly Val Leu Leu Leu
                405                 410                 415

atc caa gtg gta cct gaa gat tat aac ttt gtg tcc att gga ctg gtg    1417
Ile Gln Val Val Pro Glu Asp Tyr Asn Phe Val Ser Ile Gly Leu Val
            420                 425                 430

atg ctg ggg aaa ttt ggg atc acc tct gcc ttc tcc atg ttg tat gtc    1465
Met Leu Gly Lys Phe Gly Ile Thr Ser Ala Phe Ser Met Leu Tyr Val
        435                 440                 445

ttc act gcg gag ctc tac cca acc ctg gtc agg aac atg gct gtg ggc    1513
Phe Thr Ala Glu Leu Tyr Pro Thr Leu Val Arg Asn Met Ala Val Gly
    450                 455                 460

atc acc tcc atg gcc tct cgg gtg ggc agc atc att gcc ccc tat ttc    1561
Ile Thr Ser Met Ala Ser Arg Val Gly Ser Ile Ile Ala Pro Tyr Phe
465                 470                 475                 480

gtt tac ctg ggc gcc tat aac aga ctc cta ccc tac atc ctc atg ggc    1609
Val Tyr Leu Gly Ala Tyr Asn Arg Leu Leu Pro Tyr Ile Leu Met Gly
                485                 490                 495

agt ctg act gtc ctc att gga atc atc acg ctt ttt ttc cct gaa agt    1657
Ser Leu Thr Val Leu Ile Gly Ile Ile Thr Leu Phe Phe Pro Glu Ser
            500                 505                 510

ttt gga gtg act cta cca gag aac ttg gag cag atg cag aaa gtg aga    1705
Phe Gly Val Thr Leu Pro Glu Asn Leu Glu Gln Met Gln Lys Val Arg
        515                 520                 525

ggg ttc aga tgt ggg aaa aaa tca aca gtc tca gtg gac aga gaa gaa    1753
Gly Phe Arg Cys Gly Lys Lys Ser Thr Val Ser Val Asp Arg Glu Glu
    530                 535                 540

agc ccc aag gtt cta ata act gca ttc taacgaggtt tccaaggcac        1800
Ser Pro Lys Val Leu Ile Thr Ala Phe
545                 550

ttggcaaact gaaaagcaga tgtatacaat gagcagggtg tgatagagca agcctgcaat  1860
```

SUBA17

cccagcgctc ttggggtgga gacagaagat caggagttca aggtcatcct tggctacagc 1920

aggagtgtaa gaccagcctg tcttaccaca agcaaccctg tctcaacaga acaaatcaaa 1980

agccttttct gctgaaaggg attaacagaa acaatgagca ccaaactgga cttgtggaga 2040

aatgcacact atctcatgaa ttctgggcca ctcttccaga tgg 2083

<210> 24
<211> 24
<212> DNA
<213> Artificial Sequence

SubA1>

<220>
<223> Description of Artificial Sequence: Artificial Synthesized Primer Sequence

<400> 24
cccatgccaa caaggacaaa aagc 24

<210> 25
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Artificial Synthesized Primer Sequence

<400> 25
acagaacaga aaagccctca gtca 24

<210> 26
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Artificial Synthesized Primer Sequence

<400> 26

tgtttttcgt gggtgtgctg atgg 24

<210> 27
<211> 557
<212> PRT
<213> Mus musculus

<400> 27

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Met Arg Asp Tyr Asp Glu Val Thr Ala Phe Leu Gly Glu Trp Gly Pro
  1               5                  10                  15

Phe Gln Arg Leu Ile Phe Phe Leu Leu Ser Ala Ser Ile Ile Pro Asn
             20                  25                  30

Gly Phe Asn Gly Met Ser Ile Val Phe Leu Ala Gly Thr Pro Glu His
         35                  40                  45

Arg Cys Leu Val Pro His Thr Val Asn Leu Ser Ser Ala Trp Arg Asn
     50                  55                  60

His Ser Ile Pro Leu Glu Thr Lys Asp Gly Arg Gln Val Pro Gln Lys
 65                  70                  75                  80

Cys Arg Arg Tyr Arg Leu Ala Thr Ile Ala Asn Phe Ser Glu Leu Gly
                 85                  90                  95

Leu Glu Pro Gly Arg Asp Val Asp Leu Glu Gln Leu Glu Gln Glu Ser
            100                 105                 110

Cys Leu Asp Gly Trp Glu Tyr Asp Lys Asp Val Phe Leu Ser Thr Ile
        115                 120                 125

Val Thr Glu Trp Asp Leu Val Cys Lys Asp Asp Trp Lys Ala Pro Leu
    130                 135                 140

Thr Thr Ser Leu Phe Phe Val Gly Val Leu Met Gly Ser Phe Ile Ser
145                 150                 155                 160

Gly Gln Leu Ser Asp Arg Phe Gly Arg Lys Asn Val Leu Phe Leu Thr
                165                 170                 175

Met Gly Met Gln Thr Gly Phe Ser Phe Leu Gln Val Phe Ser Val Asn
            180                 185                 190
```

Phe Glu Met Phe Thr Val Leu Phe Val Leu Val Gly Met Gly Gln Ile
195 200 205

Ser Asn Tyr Val Ala Ala Phe Val Leu Gly Thr Glu Ile Leu Ser Lys
210 215 220

Ser Ile Arg Ile Ile Phe Ala Thr Leu Gly Val Cys Ile Phe Tyr Ala
225 230 235 240

Phe Gly Phe Met Val Leu Pro Leu Phe Ala Tyr Phe Ile Arg Asp Trp
245 250 255

SubA1

Arg Met Leu Leu Leu Ala Leu Thr Val Pro Gly Val Leu Cys Gly Ala
260 265 270

Leu Trp Trp Phe Ile Pro Glu Ser Pro Arg Trp Leu Ile Ser Gln Gly
275 280 285

A

Arg Ile Lys Glu Ala Glu Val Ile Ile Arg Lys Ala Ala Lys Ile Asn
290 295 300

Gly Ile Val Ala Pro Ser Thr Ile Phe Asp Pro Ser Glu Leu Gln Asp
305 310 315 320

Leu Asn Ser Thr Lys Pro Gln Leu His His Ile Tyr Asp Leu Ile Arg
325 330 335

Thr Arg Asn Ile Arg Val Ile Thr Ile Met Ser Ile Ile Leu Trp Leu
340 345 350

Thr Ile Ser Val Gly Tyr Phe Gly Leu Ser Leu Asp Thr Pro Asn Leu
355 360 365

His Gly Asp Ile Tyr Val Asn Cys Phe Leu Leu Ala Ala Val Glu Val
370 375 380

Pro Ala Tyr Val Leu Ala Trp Leu Leu Leu Gln Tyr Leu Pro Arg Arg
385 390 395 400

Tyr Ser Ile Ser Ala Ala Leu Phe Leu Gly Gly Ser Val Leu Leu Phe
405 410 415

```
Met Gln Leu Val Pro Ser Glu Leu Phe Tyr Leu Ser Thr Ala Leu Val
            420                 425                 430

Met Val Gly Lys Phe Gly Ile Thr Ser Ala Tyr Ser Met Val Tyr Val
        435                 440                 445

Tyr Thr Ala Glu Leu Tyr Pro Thr Val Val Arg Asn Met Gly Val Gly
    450                 455                 460

Val Ser Ser Thr Ala Ser Arg Leu Gly Ser Ile Leu Ser Pro Tyr Phe
465                 470                 475                 480

Val Tyr Leu Gly Ala Tyr Asp Arg Phe Leu Pro Tyr Ile Leu Met Gly
                485                 490                 495

Ser Leu Thr Ile Leu Thr Ala Ile Leu Thr Leu Phe Phe Pro Glu Ser
            500                 505                 510

Phe Gly Val Pro Leu Pro Asp Thr Ile Asp Gln Met Leu Arg Val Lys
        515                 520                 525

Gly Ile Lys Gln Trp Gln Ile Gln Ser Gln Thr Arg Met Gln Lys Asp
    530                 535                 540

Gly Glu Glu Ser Pro Thr Val Leu Lys Ser Thr Ala Phe
545                 550                 555
```

<210> 28
<211> 1888
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (60)..(1730)

<400> 28
ctcccgcgcc acggtgtccc cttattccca tacgggcgct gtgggaggct gaggacggc 59

atg cgg gac tac gac gag gtg acc gcc ttc cta ggc gag tgg ggg ccc 107
Met Arg Asp Tyr Asp Glu Val Thr Ala Phe Leu Gly Glu Trp Gly Pro
  1   5   10   15

```
ttc cag cgc ctc atc ttc ttc ctg ctc agc gcc agc atc atc ccc aat      155
Phe Gln Arg Leu Ile Phe Phe Leu Leu Ser Ala Ser Ile Ile Pro Asn
            20                  25                  30

ggc ttc aat ggt atg tcc atc gtg ttc ctg gcg ggg acc ccg gag cac      203
Gly Phe Asn Gly Met Ser Ile Val Phe Leu Ala Gly Thr Pro Glu His
        35                  40                  45

cgt tgc ctt gtg cct cac acc gtg aac ctg agc agc gcg tgg cgc aac      251
Arg Cys Leu Val Pro His Thr Val Asn Leu Ser Ser Ala Trp Arg Asn
    50                  55                  60

cac agt atc ccg ttg gag acg aag gac gga cga cag gtg cct cag aaa      299
His Ser Ile Pro Leu Glu Thr Lys Asp Gly Arg Gln Val Pro Gln Lys
65                  70                  75                  80

tgc cgc cgc tac cga ctg gcc acc atc gcc aac ttc tct gag cta ggg      347
Cys Arg Arg Tyr Arg Leu Ala Thr Ile Ala Asn Phe Ser Glu Leu Gly
                85                  90                  95

ctg gag ccg ggg cgg gac gtg gac ctg gag cag ctg gag cag gag agc      395
Leu Glu Pro Gly Arg Asp Val Asp Leu Glu Gln Leu Glu Gln Glu Ser
            100                 105                 110

tgc ctg gat ggc tgg gag tac gac aag gac gtc ttc ctg tcc acc atc      443
Cys Leu Asp Gly Trp Glu Tyr Asp Lys Asp Val Phe Leu Ser Thr Ile
        115                 120                 125

gtg aca gag tgg gac ctg gtg tgt aag gat gac tgg aaa gcc cca ctc      491
Val Thr Glu Trp Asp Leu Val Cys Lys Asp Asp Trp Lys Ala Pro Leu
    130                 135                 140

acc acc tcc ttg ttt ttc gtg ggt gtg ctg atg ggc tcc ttc att tca      539
Thr Thr Ser Leu Phe Phe Val Gly Val Leu Met Gly Ser Phe Ile Ser
145                 150                 155                 160

gga cag ctc tca gac agg ttt ggt cgc aag aat gtg ctg ttt ttg acc      587
Gly Gln Leu Ser Asp Arg Phe Gly Arg Lys Asn Val Leu Phe Leu Thr
                165                 170                 175

atg ggc atg cag act ggc ttc agc ttc ctg cag gtc ttc tct gtg aac      635
Met Gly Met Gln Thr Gly Phe Ser Phe Leu Gln Val Phe Ser Val Asn
            180                 185                 190
```

```
ttc gag atg ttt aca gtg ctt ttt gtc ctt gtt ggc atg ggt cag atc      683
Phe Glu Met Phe Thr Val Leu Phe Val Leu Val Gly Met Gly Gln Ile
        195                 200                 205

tcc aac tac gtg gca gca ttt gtc ctg gga aca gaa att ctt tcc aag      731
Ser Asn Tyr Val Ala Ala Phe Val Leu Gly Thr Glu Ile Leu Ser Lys
    210                 215                 220

tca att cga att ata ttc gcc acc tta gga gtt tgc ata ttt tat gcg      779
Ser Ile Arg Ile Ile Phe Ala Thr Leu Gly Val Cys Ile Phe Tyr Ala
225                 230                 235                 240

ttt ggc ttc atg gtg ctg cca ctg ttt gca tac ttc atc aga gac tgg      827
Phe Gly Phe Met Val Leu Pro Leu Phe Ala Tyr Phe Ile Arg Asp Trp
                245                 250                 255

agg atg ctg ctg ctg gcg ctc act gtg cca ggg gtg cta tgt ggg gct      875
Arg Met Leu Leu Leu Ala Leu Thr Val Pro Gly Val Leu Cys Gly Ala
            260                 265                 270

ctc tgg tgg ttc atc cct gag tcc cca cga tgg ctc atc tct caa ggc      923
Leu Trp Trp Phe Ile Pro Glu Ser Pro Arg Trp Leu Ile Ser Gln Gly
        275                 280                 285

cga att aaa gag gca gag gtg atc atc cgc aaa gct gcc aaa atc aat      971
Arg Ile Lys Glu Ala Glu Val Ile Ile Arg Lys Ala Ala Lys Ile Asn
    290                 295                 300

ggg att gtt gca cct tcc act atc ttc gat cca agt gag tta caa gac     1019
Gly Ile Val Ala Pro Ser Thr Ile Phe Asp Pro Ser Glu Leu Gln Asp
305                 310                 315                 320

tta aat tct acg aag cct cag ttg cac cac att tat gat ctg atc cga     1067
Leu Asn Ser Thr Lys Pro Gln Leu His His Ile Tyr Asp Leu Ile Arg
                325                 330                 335

aca cgg aat atc agg gtc atc acc atc atg tct ata atc ctg tgg ctg     1115
Thr Arg Asn Ile Arg Val Ile Thr Ile Met Ser Ile Ile Leu Trp Leu
            340                 345                 350

acc ata tca gtg ggc tat ttt gga cta tct ctt gac act cct aac ttg     1163
Thr Ile Ser Val Gly Tyr Phe Gly Leu Ser Leu Asp Thr Pro Asn Leu
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SubA1

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        355                 360                 365

cat ggg gac atc tat gtg aac tgc ttc cta ctg gcg gct gtt gaa gtc    1211
His Gly Asp Ile Tyr Val Asn Cys Phe Leu Leu Ala Ala Val Glu Val
    370                 375                 380

cca gcc tat gtg ctg gcc tgg ctg ttg ttg cag tac ttg ccc cgg cga    1259
Pro Ala Tyr Val Leu Ala Trp Leu Leu Leu Gln Tyr Leu Pro Arg Arg
385                 390                 395                 400

tat tct atc tcg gct gcc ctt ttc ctg ggt ggc agt gtc ctt ctc ttc    1307
Tyr Ser Ile Ser Ala Ala Leu Phe Leu Gly Gly Ser Val Leu Leu Phe
                405                 410                 415

atg cag ctg gtg cct tca gaa ttg ttt tac ttg tcc act gcc ctg gtg    1355
Met Gln Leu Val Pro Ser Glu Leu Phe Tyr Leu Ser Thr Ala Leu Val
            420                 425                 430

atg gtg ggg aag ttt gga atc acc tct gcc tac tcc atg gtc tat gtg    1403
Met Val Gly Lys Phe Gly Ile Thr Ser Ala Tyr Ser Met Val Tyr Val
        435                 440                 445

tac aca gct gag ctg tac ccc act gtg gtc aga aac atg ggt gtg ggg    1451
Tyr Thr Ala Glu Leu Tyr Pro Thr Val Val Arg Asn Met Gly Val Gly
    450                 455                 460

gtc agc tcc aca gca tcc cgc ctt ggc agc atc ctg tct ccc tac ttt    1499
Val Ser Ser Thr Ala Ser Arg Leu Gly Ser Ile Leu Ser Pro Tyr Phe
465                 470                 475                 480

gtt tac cta ggt gcc tat gat cgc ttc ctg cct tat att ctc atg gga    1547
Val Tyr Leu Gly Ala Tyr Asp Arg Phe Leu Pro Tyr Ile Leu Met Gly
                485                 490                 495

agt ctg acc atc ctg aca gct atc ctc acc ttg ttc ttc cct gag agc    1595
Ser Leu Thr Ile Leu Thr Ala Ile Leu Thr Leu Phe Phe Pro Glu Ser
            500                 505                 510

ttt ggt gtc cct ctc cca gat acc att gac cag atg cta agg gtc aaa    1643
Phe Gly Val Pro Leu Pro Asp Thr Ile Asp Gln Met Leu Arg Val Lys
        515                 520                 525

gga ata aaa cag tgg caa atc caa agc cag aca aga atg caa aaa gat    1691
```

SUBA1

Gly Ile Lys Gln Trp Gln Ile Gln Ser Gln Thr Arg Met Gln Lys Asp
530 535 540

Sub A1

ggt gaa gaa agc cca aca gtc cta aag agc aca gcc ttc taacaccctg 1740
Gly Glu Glu Ser Pro Thr Val Leu Lys Ser Thr Ala Phe
545 550 555

tccagaaggc aaaaaactga ttggaaacct tcatgttgtc agaaatgctc tccatgactg 1800

agggcttttc tgttctgtta accttgtgtc taacatgctc atggattggg gcatctgtcc 1860

tggagagtca ccttcctcta gggacacc 1888

SEQ ID NO:29

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SEQ ID NO:30

TGTAGCGTGAAGACGACAGAAAGGGCGTGGTGCGGAGGGCGGT

SEQ ID NO:31

acctgcccgg

SEQ ID NO:32

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